SEQUENCE LISTING

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<120> Methods of Diagnosing & Treating Diabetes and Insulin Resistance

<130> 016325-013600PC

<140> WO PCT/US03/18046
<141> 2003-06-05

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<151> 2002-06-05

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Ser Gly Cys Leu Cys Pro Pro Leu Asn Val Asn Glu Glu Tyr Ile Ile
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Met Gly Tyr Glu Asp Glu Glu Arg Ser Arg Leu Leu Leu Val Glu Gly
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Ser Pro Asp Leu Leu Phe Phe Leu Cys Ala Met Tyr Ala Pro Ile Cys
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Thr Ile Asp Phe Gln His Glu Pro Ile Lys Pro Cys Lys Ser Val Cys
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Glu Arg Ala Arg Gln Gly Cys Glu Pro Ile Leu Ile Lys Tyr Arg His
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Ser Trp Pro Glu Ser Leu Ala Cys Asp Glu Leu Pro Val Tyr Asp Arg
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Phe Pro Met Asp Ser Ser Thr Gly His Cys Arg Gly Ala Ser Ser Glu
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Arg Cys Lys Cys Lys Pro Val Arg Ala Thr Gln Lys Thr Tyr Phe Arg
            180                 185                 190

Asn Asn Tyr Asn Tyr Val Ile Arg Ala Lys Val Lys Glu Val Lys Met
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Lys Cys His Asp Val Thr Ala Val Val Glu Val Lys Glu Ile Leu Lys
    210                 215                 220

Ala Ser Leu Val Asn Ile Pro Arg Asp Thr Val Asn Leu Tyr Thr Thr
225                 230                 235                 240

Ser Gly Cys Leu Cys Pro Pro Leu Thr Val Asn Glu Glu Tyr Val Ile
                245                 250                 255

Met Gly Tyr Glu Asp Glu Glu Arg Ser Arg Leu Leu Leu Val Glu Gly
            260                 265                 270

Ser Ile Ala Glu Lys Trp Lys Asp Arg Leu Gly Lys Lys Val Lys Arg
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Trp Asp Met Lys Leu Arg His Leu Gly Leu Gly Lys Thr Asp Ala Ser
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Lys Lys Lys Asp Arg Phe Tyr Arg Ser Ile Leu Pro Gly Asp Lys Thr
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Val Ile His Arg Asp Ile Lys Ser Asp Asn Ile Leu Leu Gly Met Asp
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Lys Glu Leu Leu Gln His Gln Phe Leu Lys Ile Ala Lys Pro Leu Ser
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Lys Lys Lys Asp Arg Phe Tyr Arg Ser Ile Leu Pro Gly Asp Lys Thr
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Asn Lys Lys Lys Glu Lys Glu Arg Pro Glu Ile Ser Leu Pro Ser Asp
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            100                 105                 110

Thr Lys Ser Glu Gln Lys Lys Asn Pro Gln Ala Val Leu Asp Val Leu
        115                 120                 125

Glu Phe Tyr Asn Ser Lys Lys Thr Ser Asn Ser Gln Lys Tyr Met Ser
    130                 135                 140

Phe Thr Asp Lys Ser Ala Glu Asp Tyr Asn Ser Ser Asn Ala Leu Asn
145                 150                 155                 160

Val Lys Ala Val Ser Glu Thr Pro Ala Val Pro Pro Val Ser Glu Asp
                165                 170                 175

Glu Asp Asp Asp Asp Asp Asp Ala Thr Pro Pro Pro Val Ile Ala Pro
            180                 185                 190

Arg Pro Glu His Thr Lys Ser Val Tyr Thr Arg Ser Val Ile Glu Pro
        195                 200                 205

Leu Pro Val Thr Pro Thr Arg Asp Val Ala Thr Ser Pro Ile Ser Pro
    210                 215                 220

Thr Glu Asn Asn Thr Thr Pro Pro Asp Ala Leu Thr Arg Asn Thr Glu
225                 230                 235                 240

Lys Gln Lys Lys Lys Pro Lys Met Ser Asp Glu Glu Ile Leu Glu Lys
                245                 250                 255

Leu Arg Ser Ile Val Ser Val Gly Asp Pro Lys Lys Lys Tyr Thr Arg
            260                 265                 270

Phe Glu Lys Ile Gly Gln Gly Ala Ser Gly Thr Val Tyr Thr Ala Met
        275                 280                 285

Asp Val Ala Thr Gly Gln Glu Val Ala Ile Lys Gln Met Asn Leu Gln
    290                 295                 300

Gln Gln Pro Lys Lys Glu Leu Ile Ile Asn Glu Ile Leu Val Met Arg
305                 310                 315                 320

Glu Asn Lys Asn Pro Asn Ile Val Asn Tyr Leu Asp Ser Tyr Leu Val
                325                 330                 335

Gly Asp Glu Leu Trp Val Val Met Glu Tyr Leu Ala Gly Gly Ser Leu
            340                 345                 350

Thr Asp Val Val Thr Glu Thr Cys Met Asp Glu Gly Gln Ile Ala Ala
        355                 360                 365

Val Cys Arg Glu Cys Leu Gln Ala Leu Glu Phe Leu His Ser Asn Gln
    370                 375                 380

Val Ile His Arg Asp Ile Lys Ser Asp Asn Ile Leu Leu Gly Met Asp
385                 390                 395                 400
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Gly Ser Val Lys Leu Thr Asp Phe Gly Phe Cys Ala Gln Ile Thr Pro
                405                 410                 415

Glu Gln Ser Lys Arg Ser Thr Met Val Gly Thr Pro Tyr Trp Met Ala
            420                 425                 430

Pro Glu Val Val Thr Arg Lys Ala Tyr Gly Pro Lys Val Asp Ile Trp
        435                 440                 445

Ser Leu Gly Ile Met Ala Ile Glu Met Ile Glu Gly Glu Pro Pro Tyr
    450                 455                 460

Leu Asn Glu Asn Pro Leu Arg Ala Leu Tyr Leu Ile Ala Thr Asn Gly
465                 470                 475                 480

Thr Pro Glu Leu Gln Asn Pro Glu Lys Leu Ser Ala Ile Phe Arg Asp
                485                 490                 495

Phe Leu Asn Arg Cys Leu Glu Met Asp Val Glu Lys Arg Gly Ser Ala
            500                 505                 510

Lys Glu Leu Leu Gln Val Arg Lys Leu Arg Phe Gln Val Phe Ser Asn
        515                 520                 525

Phe Ser Met Ile Ala Ala Ser Ile Pro Glu Asp Cys Gln Ala Pro Leu
    530                 535                 540

Gln Pro His Ser Thr Asp Cys Cys Ser
545                 550
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<210> 9
<211> 1347
<212> DNA
<213> Homo sapiens

<220>
<223> human p21 activated kinase 1B (PAK1B) new splice variant

<400> 9
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cctccaaacc cagaggagaa gaaaaagaag gaccgatttt accgatccat tttacctgga 180
gataaaacaa ataaaaagaa agagaaagag cggccagaga tttctctccc ttcagatttt 240
gaacacacaa ttcatgtcgg ttttgatgct gtcacagggg agtttacggg aatgccagag 300
cagtgggccc gcttgcttca gacatcaaat atcactaagt cggagcagaa gaaaaacccg 360
caggctgttc tggatgtgtt ggagttttac aactcgaaga agacatccaa cagccagaaa 420
tacatgagct ttacagataa gtcagctgag gattacaatt cttctaatgc cttgaatgtg 480
aaggctgtgt ctgagactcc tgcagtgcca ccagtttcag aagatgagga tgatgatgat 540
gatgatgcta ccccaccacc agtgattgct ccacgcccag agcacacaaa atctgtggcc 600
attaagcaga tgaatcttca gcagcagccc aagaaagagc tgattattaa tgagatcctg 660
gtcatgaggg aaaacaagaa cccaaacatt gtgaattact tggacagtta cctcgtggga 720
gatgagctgt gggttgttat ggaatacttg gctggaggct ccttgacaga tgtggtgaca 780
gaaacttgca tggatgaagg ccaaattgca gctgtgtgcc gtgagtgtct gcaggctctg 840
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cgaaaggcct atgggcccaa ggttgacatc tggtccctgg gcatcatggc catcgaaatg 1080
attgaagggg agcctccata cctcaatgaa aaccctctga gagccttgta cctcattgcc 1140
accaatggga ccccagaact tcagaaccca gagaagctgt cagctatctt ccgggacttt 1200

ctgaaccgct gtctcgggat ggatgtggag aagagaggtt cagctaaaga gctgctacag 1260
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aaggaggcaa caaagaacaa tcactaa 1347

<210> 10
<211> 449
<212> PRT
<213> Homo sapiens

<220>
<223> human p21 activated kinase 1B (PAK1B) new splice variant

<400> 10
Met Ser Asn Asn Gly Leu Asp Ile Gln Asp Lys Pro Pro Ala Pro Pro
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Met Arg Asn Thr Ser Thr Met Ile Gly Ala Gly Ser Lys Asp Ala Gly
20 25 30

Thr Leu Asn His Gly Ser Lys Pro Leu Pro Pro Asn Pro Glu Glu Lys
35 40 45

Lys Lys Lys Asp Arg Phe Tyr Arg Ser Ile Leu Pro Gly Asp Lys Thr
50 55 60

Asn Lys Lys Lys Glu Lys Glu Arg Pro Glu Ile Ser Leu Pro Ser Asp
65 70 75 80

Phe Glu His Thr Ile His Val Gly Phe Asp Ala Val Thr Gly Glu Phe
85 90 95

Thr Gly Met Pro Glu Gln Trp Ala Arg Leu Leu Gln Thr Ser Asn Ile
100 105 110

Thr Lys Ser Glu Gln Lys Lys Asn Pro Gln Ala Val Leu Asp Val Leu
115 120 125

Glu Phe Tyr Asn Ser Lys Lys Thr Ser Asn Ser Gln Lys Tyr Met Ser
130 135 140

Phe Thr Asp Lys Ser Ala Glu Asp Tyr Asn Ser Ser Asn Ala Leu Asn
145 150 155 160

Val Lys Ala Val Ser Glu Thr Pro Ala Val Pro Pro Val Ser Glu Asp
165 170 175

Glu Asp Asp Asp Asp Asp Asp Ala Thr Pro Pro Pro Val Ile Ala Pro
180 185 190

Arg Pro Glu His Thr Lys Ser Val Ala Ile Lys Gln Met Asn Leu Gln
195 200 205

Gln Gln Pro Lys Lys Glu Leu Ile Ile Asn Glu Ile Leu Val Met Arg
210 215 220

Glu Asn Lys Asn Pro Asn Ile Val Asn Tyr Leu Asp Ser Tyr Leu Val
225 230 235 240

```
Gly Asp Glu Leu Trp Val Val Met Glu Tyr Leu Ala Gly Gly Ser Leu
                245                 250                 255

Thr Asp Val Val Thr Glu Thr Cys Met Asp Glu Gly Gln Ile Ala Ala
            260                 265                 270

Val Cys Arg Glu Cys Leu Gln Ala Leu Glu Phe Leu His Ser Asn Gln
        275                 280                 285

Val Ile His Arg Asp Ile Lys Ser Asp Asn Ile Leu Leu Gly Met Asp
    290                 295                 300

Gly Ser Val Lys Leu Thr Asp Phe Gly Phe Cys Ala Gln Ile Thr Pro
305                 310                 315                 320

Glu Gln Ser Lys Arg Ser Thr Met Val Gly Thr Pro Tyr Trp Met Ala
                325                 330                 335

Pro Glu Val Val Thr Arg Lys Ala Tyr Gly Pro Lys Val Asp Ile Trp
            340                 345                 350

Ser Leu Gly Ile Met Ala Ile Glu Met Ile Glu Gly Glu Pro Pro Tyr
        355                 360                 365

Leu Asn Glu Asn Pro Leu Arg Ala Leu Tyr Leu Ile Ala Thr Asn Gly
    370                 375                 380

Thr Pro Glu Leu Gln Asn Pro Glu Lys Leu Ser Ala Ile Phe Arg Asp
385                 390                 395                 400

Phe Leu Asn Arg Cys Leu Gly Met Asp Val Glu Lys Arg Gly Ser Ala
                405                 410                 415

Lys Glu Leu Leu Gln His Gln Phe Leu Lys Ile Ala Lys Pro Leu Ser
            420                 425                 430

Ser Leu Thr Pro Leu Ile Ala Ala Ala Lys Glu Ala Thr Lys Asn Asn
        435                 440                 445

His
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<210> 11
<211> 1977
<212> DNA
<213> Mus musculus

<220>
<223> mouse p21 (CDKN1A)-activated kinase 1B (PAK1B)
cDNA

<220>
<221> CDS
<222> (190)..(1827)
<223> PAK1B

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cgagactcac agatacacaa gatcacgccc cgcacccacc gccagtagct gctgctgctg 180
gtggtgacaa tgtcaaataa cggcgtagac atccaggaca aacccccagc ccctccgatg 240

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atcttacctg gagataaaac aaataaaaag agggagaagg agcgaccaga gatttctctt 420
ccttcagatt ttgagcatac aattcatgtt ggttttgatg ctgtcacagg ggagtttacg 480
ggaatgccag aacagtgggc tcgcttgctt caaacatcaa atatcacaaa gtcagagcag 540
aagaaaaacc cacaggctgt tctggatgtg ttggaatttt ataactctaa gaagacctcc 600
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gaagatgatg atgacgatgc taccccacct ccagtgattg ctccacgccc agaacacaca 780
aaatctgtat atacacgatc tgtgattgaa ccacttcctg ttactccaac tcgggatgtg 840
gctacatctc ctatttctcc tactgagaat aacaccactc cgccagatgc tttgacccgg 900
aacacggaaa aacagaagaa gaagcctaaa atgtctgatg aggagatctt agagaaatta 960
cggagcatag tgagtgtggg tgaccccaag aagaagtaca caccgttcga gaagattgga 1020
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attaaacaga tgaatcttca gcagcagccg aagaaagagc tgattattaa tgagatcctg 1140
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gatgagctgt gggttgttat ggaatacttg gctggaggct ccttgacaga tgtggtgaca 1260
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<210> 12
<211> 545
<212> PRT
<213> Mus musculus

<220>
<223> mouse p21 (CDKN1A)-activated kinase 1B (PAK1B)

<400> 12

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Met Ser Asn Asn Gly Val Asp Ile Gln Asp Lys Pro Pro Ala Pro Pro
  1               5                  10                  15

Met Arg Asn Thr Ser Thr Met Ile Gly Ala Gly Ser Lys Asp Thr Gly
             20                  25                  30

Thr Leu Asn His Gly Ser Lys Pro Leu Pro Pro Asn Pro Glu Glu Lys
         35                  40                  45

Lys Lys Lys Asp Arg Phe Tyr Arg Ser Ile Leu Pro Gly Asp Lys Thr
     50                  55                  60

Asn Lys Lys Arg Glu Lys Glu Arg Pro Glu Ile Ser Leu Pro Ser Asp
 65                  70                  75                  80

Phe Glu His Thr Ile His Val Gly Phe Asp Ala Val Thr Gly Glu Phe
                 85                  90                  95

Thr Gly Met Pro Glu Gln Trp Ala Arg Leu Leu Gln Thr Ser Asn Ile
            100                 105                 110
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Thr Lys Ser Glu Gln Lys Lys Asn Pro Gln Ala Val Leu Asp Val Leu
        115                 120                 125

Glu Phe Tyr Asn Ser Lys Lys Thr Ser Asn Ser Lys Lys Tyr Met Ser
    130                 135                 140

Phe Thr Asp Lys Ser Ala Glu Asp Tyr Asn Ser Ser Asn Thr Leu Asn
145                 150                 155                 160

Val Lys Thr Val Ser Glu Thr Pro Ala Val Pro Pro Val Ser Glu Asp
                165                 170                 175

Asp Glu Asp Asp Asp Asp Asp Ala Thr Pro Pro Pro Val Ile Ala Pro
            180                 185                 190

Arg Pro Glu His Thr Lys Ser Val Tyr Thr Arg Ser Val Ile Glu Pro
        195                 200                 205

Leu Pro Val Thr Pro Thr Arg Asp Val Ala Thr Ser Pro Ile Ser Pro
    210                 215                 220

Thr Glu Asn Asn Thr Thr Pro Pro Asp Ala Leu Thr Arg Asn Thr Glu
225                 230                 235                 240

Lys Gln Lys Lys Lys Pro Lys Met Ser Asp Glu Glu Ile Leu Glu Lys
                245                 250                 255

Leu Arg Ser Ile Val Ser Val Gly Asp Pro Lys Lys Lys Tyr Thr Pro
            260                 265                 270

Phe Glu Lys Ile Gly Gln Gly Ala Ser Gly Thr Val Tyr Thr Ala Met
        275                 280                 285

Asp Val Ala Thr Gly Gln Glu Val Ala Ile Lys Gln Met Asn Leu Gln
    290                 295                 300

Gln Gln Pro Lys Lys Glu Leu Ile Ile Asn Glu Ile Leu Val Met Arg
305                 310                 315                 320

Glu Asn Lys Asn Pro Asn Ile Val Asn Tyr Leu Asp Ser Tyr Leu Val
                325                 330                 335

Gly Asp Glu Leu Trp Val Val Met Glu Tyr Leu Ala Gly Gly Ser Leu
            340                 345                 350

Thr Asp Val Val Thr Glu Thr Cys Met Asp Glu Gly Gln Ile Ala Ala
        355                 360                 365

Val Cys Arg Glu Cys Leu Gln Ala Leu Glu Phe Leu His Ser Asn Gln
    370                 375                 380

Val Ile His Arg Asp Ile Lys Ser Asp Asn Ile Leu Leu Gly Met Asp
385                 390                 395                 400

Gly Ser Val Lys Leu Thr Asp Phe Gly Phe Cys Ala Gln Ile Thr Pro
                405                 410                 415

Glu Gln Ser Lys Arg Ser Thr Met Val Gly Thr Pro Tyr Trp Met Ala
            420                 425                 430
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Pro Glu Val Val Thr Arg Lys Ala Tyr Gly Pro Lys Val Asp Ile Trp
        435                 440                 445

Ser Leu Gly Ile Met Ala Ile Glu Met Ile Glu Gly Glu Pro Pro Tyr
    450                 455                 460

Leu Asn Glu Asn Pro Leu Arg Ala Leu Tyr Leu Ile Ala Thr Asn Gly
465                 470                 475                 480

Thr Pro Glu Leu Gln Asn Pro Glu Lys Leu Ser Ala Ile Phe Arg Asp
                485                 490                 495

Phe Leu Gln Cys Cys Leu Glu Met Asp Val Glu Lys Arg Gly Ser Ala
            500                 505                 510

Lys Glu Leu Leu Gln His Gln Phe Leu Lys Ile Ala Lys Pro Leu Ser
        515                 520                 525

Ser Leu Thr Pro Leu Met His Ala Ala Lys Glu Ala Thr Lys Asn Asn
    530                 535                 540

His
545
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<210> 13
<211> 2539
<212> DNA
<213> Rattus norvegicus

<220>
<223> rat p21 (CDKN1A)-activated kinase 1B (PAK1B) cDNA

<220>
<221> CDS
<222> (389)..(2023)
<223> PAK1B

<400> 13
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gcggccagag atttctcttc cttcagattt tgagcataca attcatgttg gttttgatgc 660
tgtcacaggg gagtttacgg ggatgccaga acagtgggcc cgcttgcttc aaacatcaaa 720
tatcaccaag tcagagcaga agaaaaaccc acaggctgtt ctggatgtgt tggaatttta 780
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agattataat tcttctaata ctttgaatgt gaagactgtg tctgagaccc cagcagtgcc 900
accagtgtca gaagatgaag atgatgatga cgatgctacc ccacctccag tgattgctcc 960
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gatcttagag aaattacgga gcatagtgag tgtgggcgat cctaagaaga agtacacacg 1200
cttcgagaag attggacaag gtgcttcagg cacagtgtac actgcaatgg atgtagccac 1260
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<210> 14
<211> 544
<212> PRT
<213> Rattus norvegicus

<220>
<223> rat p21 (CDKN1A)-activated kinase 1B (PAK1B)

<400> 14

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Met Ser Asn Asn Gly Leu Asp Val Gln Asp Lys Pro Pro Ala Pro Pro
  1               5                  10                  15

Met Arg Asn Thr Ser Thr Met Ile Gly Ala Gly Ser Lys Asp Pro Gly
             20                  25                  30

Thr Leu Asn His Gly Ser Lys Pro Leu Pro Pro Asn Pro Glu Glu Lys
         35                  40                  45

Lys Lys Lys Asp Arg Phe Tyr Arg Ser Ile Leu Ala Gly Asp Lys Thr
     50                  55                  60

Asn Lys Lys Lys Glu Lys Glu Arg Pro Glu Ile Ser Leu Pro Ser Asp
 65                  70                  75                  80

Phe Glu His Thr Ile His Val Gly Phe Asp Ala Val Thr Gly Glu Phe
                 85                  90                  95

Thr Gly Met Pro Glu Gln Trp Ala Arg Leu Leu Gln Thr Ser Asn Ile
            100                 105                 110

Thr Lys Ser Glu Gln Lys Lys Asn Pro Gln Ala Val Leu Asp Val Leu
        115                 120                 125

Glu Phe Tyr Asn Ser Lys Lys Thr Ser Asn Ser Gln Lys Tyr Met Ser
    130                 135                 140

Phe Thr Asp Lys Ser Ala Glu Asp Tyr Asn Ser Ser Asn Thr Leu Asn
145                 150                 155                 160
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Val Lys Thr Val Ser Glu Thr Pro Ala Val Pro Pro Val Ser Glu Asp
165 170 175

Glu Asp Asp Asp Asp Asp Ala Thr Pro Pro Pro Val Ile Ala Pro Arg
180 185 190

Pro Glu His Thr Lys Ser Val Tyr Thr Arg Ser Val Ile Glu Pro Leu
195 200 205

Pro Val Thr Pro Thr Arg Asp Val Ala Thr Ser Pro Ile Ser Pro Thr
210 215 220

Glu Asn Asn Thr Thr Pro Pro Asp Ala Leu Thr Arg Asn Thr Glu Lys
225 230 235 240

Gln Lys Lys Lys Pro Lys Met Ser Asp Glu Glu Ile Leu Glu Lys Leu
245 250 255

Arg Ser Ile Val Ser Val Gly Asp Pro Lys Lys Lys Tyr Thr Arg Phe
260 265 270

Glu Lys Ile Gly Gln Gly Ala Ser Gly Thr Val Tyr Thr Ala Met Asp
275 280 285

Val Ala Thr Gly Gln Glu Val Ala Ile Lys Gln Met Asn Leu Gln Gln
290 295 300

Gln Pro Lys Lys Glu Leu Ile Ile Asn Glu Ile Leu Val Met Arg Glu
305 310 315 320

Asn Lys Asn Pro Asn Ile Val Asn Tyr Leu Asp Ser Tyr Leu Val Gly
325 330 335

Asp Glu Leu Trp Val Val Met Glu Tyr Leu Ala Gly Gly Ser Leu Thr
340 345 350

Asp Val Val Thr Glu Thr Cys Met Asp Glu Gly Gln Ile Ala Ala Val
355 360 365

Cys Arg Glu Cys Leu Gln Ala Leu Glu Phe Leu His Ser Asn Gln Val
370 375 380

Ile His Arg Asp Ile Lys Ser Asp Asn Ile Leu Leu Gly Met Asp Gly
385 390 395 400

Ser Val Lys Leu Thr Asp Phe Gly Phe Cys Ala Gln Ile Thr Pro Glu
405 410 415

Gln Ser Lys Arg Ser Thr Met Val Gly Thr Pro Tyr Trp Met Ala Pro
420 425 430

Glu Val Val Thr Arg Lys Ala Tyr Gly Pro Lys Val Asp Ile Trp Ser
435 440 445

Leu Gly Ile Met Ala Ile Glu Met Ile Glu Gly Glu Pro Pro Tyr Leu
450 455 460

Asn Glu Asn Pro Leu Arg Ala Leu Tyr Leu Ile Ala Thr Asn Gly Thr
465 470 475 480

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Pro Glu Leu Gln Asn Pro Glu Lys Leu Ser Ala Ile Phe Arg Asp Phe
                485                 490                 495

Leu Asn Arg Cys Leu Glu Met Asp Val Glu Lys Arg Gly Ser Ala Lys
            500                 505                 510

Glu Leu Leu Gln His Gln Phe Leu Lys Ile Ala Lys Pro Leu Ser Ser
        515                 520                 525

Leu Thr Pro Leu Ile Ala Ala Ala Lys Glu Ala Thr Lys Asn Asn His
    530                 535                 540
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<210> 15
<211> 1662
<212> DNA
<213> Homo sapiens

<220>
<223> human SPUVE serine protease 23 cDNA

<220>
<221> CDS
<222> (121)..(1272)
<223> SPUVE

<400> 15
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gatggtggtc gaggggccaa cgactccact tcagccatgc ccgagcagat gaaatttcag 780
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<210> 16
<211> 383
<212> PRT
<213> Homo sapiens

<220>
<223> human SPUVE serine protease 23

<400> 16
Met Ala Gly Ile Pro Gly Leu Leu Phe Leu Leu Phe Phe Leu Leu Cys
1 5 10 15

Ala Val Gly Gln Val Ser Pro Tyr Ser Ala Pro Trp Lys Pro Thr Trp
20 25 30

Pro Ala Tyr Arg Leu Pro Val Val Leu Pro Gln Ser Thr Leu Asn Leu
35 40 45

Ala Lys Pro Asp Phe Gly Ala Glu Ala Lys Leu Glu Val Ser Ser Ser
50 55 60

Cys Gly Pro Gln Cys His Lys Gly Thr Pro Leu Pro Thr Tyr Glu Glu
65 70 75 80

Ala Lys Gln Tyr Leu Ser Tyr Glu Thr Leu Tyr Ala Asn Gly Ser Arg
85 90 95

Thr Glu Thr Gln Val Gly Ile Tyr Ile Leu Ser Ser Ser Gly Asp Gly
100 105 110

Ala Gln His Arg Asp Ser Gly Ser Ser Gly Lys Ser Arg Arg Lys Arg
115 120 125

Gln Ile Tyr Gly Tyr Asp Ser Arg Phe Ser Ile Phe Gly Lys Asp Phe
130 135 140

Leu Leu Asn Tyr Pro Phe Ser Thr Ser Val Lys Leu Ser Thr Gly Cys
145 150 155 160

Thr Gly Thr Leu Val Ala Glu Lys His Val Leu Thr Ala Ala His Cys
165 170 175

Ile His Asp Gly Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val
180 185 190

Gly Phe Leu Lys Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp
195 200 205

Ser Thr Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val
210 215 220

Lys Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp
225 230 235 240

Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro His
245 250 255

Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys Gln Leu
260 265 270

Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp Arg Pro Gly
275 280 285

Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu Thr Tyr Asp Leu
290 295 300

```
Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala Ser Gly Ser Gly Val
305                 310                 315                 320

Tyr Val Arg Met Trp Lys Arg Gln Gln Gln Lys Trp Glu Arg Lys Ile
                325                 330                 335

Ile Gly Ile Phe Ser Gly His Gln Trp Val Asp Met Asn Gly Ser Pro
            340                 345                 350

Gln Asp Phe Asn Val Ala Val Arg Ile Thr Pro Leu Lys Tyr Ala Gln
        355                 360                 365

Ile Cys Tyr Trp Ile Lys Gly Asn Tyr Leu Asp Cys Arg Glu Gly
    370                 375                 380


<210> 17
<211> 1936
<212> DNA
<213> Mus musculus

<220>
<223> mouse SPUVE serine protease 23 cDNA

<220>
<221> CDS
<222> (170)..(1318)
<223> SPUVE

<400> 17
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cgttccgtgg aaacccacat ggccggctta tcgcctccct gtagtcttgc ctcagtctac 300
cctcaactta gctaaggcag acttcgacgc caaagcgaaa ttggaggtgt cctcctcatg 360
tggacctcag tgtcacaagg gaacaccact gcccacctac gaagaggcca agcagtacct 420
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cctcagcaat ggtgaaggca gggcacgagg cagagactcg gaggccacag ggagatctcg 540
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ccggcccggc aatttggtgt accgcttctg tgatgtcaaa gatgagacct acgaccttct 1080
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caaaaattat tggctatatt attttaaaac tgttgtgtgc gttatagcat ttaagcagtc 1500
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atgttttctt ctgagagtca tatattgata tttttgtaat gtgtggttat tatgcttcca 1740
gataatgata gcaaagtctt caataggcaa tttataatgt tttggattca aacatttacg 1800
tagtagtcct tgaagagaac aataatttat tggctatatt gatacccata taagactgta 1860
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aaaaaaaaaa aaaaaa 1936

<210> 18
<211> 382
<212> PRT
<213> Mus musculus

<220>
<223> mouse SPUVE serine protease 23

<400> 18
Met Ala Gly Ile Pro Gly Leu Phe Ile Leu Leu Val Leu Leu Cys Val
1 5 10 15

Phe Met Gln Val Ser Pro Tyr Thr Val Pro Trp Lys Pro Thr Trp Pro
20 25 30

Ala Tyr Arg Leu Pro Val Val Leu Pro Gln Ser Thr Leu Asn Leu Ala
35 40 45

Lys Ala Asp Phe Asp Ala Lys Ala Lys Leu Glu Val Ser Ser Ser Cys
50 55 60

Gly Pro Gln Cys His Lys Gly Thr Pro Leu Pro Thr Tyr Glu Glu Ala
65 70 75 80

Lys Gln Tyr Leu Ser Tyr Glu Thr Leu Tyr Ala Asn Gly Ser Arg Thr
85 90 95

Glu Thr Arg Val Gly Ile Tyr Ile Leu Ser Asn Gly Glu Gly Arg Ala
100 105 110

Arg Gly Arg Asp Ser Glu Ala Thr Gly Arg Ser Arg Arg Lys Arg Gln
115 120 125

Ile Tyr Gly Tyr Asp Gly Arg Phe Ser Ile Phe Gly Lys Asp Phe Leu
130 135 140

Leu Asn Tyr Pro Phe Ser Thr Ser Val Lys Leu Ser Thr Gly Cys Thr
145 150 155 160

Gly Thr Leu Val Ala Glu Lys His Val Leu Thr Ala Ala His Cys Ile
165 170 175

His Asp Gly Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val Gly
180 185 190

Phe Leu Lys Pro Lys Tyr Lys Asp Gly Ala Gly Gly Asp Asn Ser Ser
195 200 205

Ser Ser Ala Met Pro Asp Lys Met Lys Phe Gln Trp Ile Arg Val Lys
210 215 220

Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp Ile
225 230 235 240

Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro His Lys
245 250 255

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Arg Gln Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys Gln Leu Pro
            260                 265                 270

Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp Arg Pro Gly Asn
        275                 280                 285

Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu Thr Tyr Asp Leu Leu
    290                 295                 300

Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala Ser Gly Ser Gly Val Tyr
305                 310                 315                 320

Val Arg Met Trp Lys Arg Pro Gln Gln Lys Trp Glu Arg Lys Ile Ile
                325                 330                 335

Gly Ile Phe Ser Gly His Gln Trp Val Asp Met Asn Gly Ser Pro Gln
            340                 345                 350

Asp Phe Asn Val Ala Val Arg Ile Thr Pro Leu Lys Tyr Ala Gln Ile
        355                 360                 365

Cys Tyr Trp Ile Lys Gly Asn Tyr Leu Asp Cys Arg Glu Gly
    370                 375                 380
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<210> 19
<211> 827
<212> DNA
<213> Homo sapiens

<220>
<223> human similar to natural killer cell transcript 4 (NK4) cDNA

<220>
<221> CDS
<222> (59)..(625)
<223> NK4

<400> 19
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catagaaaga ttttatgata aaatgcaaaa tgcagaatca ggacgtggac aggtgatgtc 180
gagcctggca gagctggagg acgacttcaa agagggctac ctggagacag tggcggctta 240
ttatgaggag cagcacccag agctcactcc tctacttgaa aaagaaagag atggattacg 300
gtgccgaggc aacagatccc ctgtcccgga tgttgaggat cccgcaaccg aggagcctgg 360
ggagagcttt tgtgacaagg tcatgagatg gttccaggcc atgctgcagc ggctgcagac 420
ctggtggcac ggggttctgg cctgggtgaa ggagaaggtg gtggccctgg tccatgcagt 480
gcaggccctc tggaaacagt tccagagttt ctgctgctct ctgtcagagc tcttcatgtc 540
ctctttccag tcctacggag ccccacgggg ggacaaggag gagctgacac cccagaagtg 600
ctctgaaccc caatcctcaa aatgaagata ctgacaccac ctttgccctc cccgtcaccg 660
cgcacccacc ctgacccctc cctcagctgt cctgtgcccc gccctctccc gcacactcag 720
tcccccctgcc tggcgttcct gccgcagctc tgacctggtg ctgtcgccct ggcatcttaa 780
taaaacctgc ttatacttcc ctggaaaaaa aaaaaaaaaa aaaaaaa 827

<210> 20
<211> 188
<212> PRT
<213> Homo sapiens

<220>
<223> human similar to natural killer cell transcript 4
(NK4)

<400> 20
Met Cys Phe Pro Lys Val Leu Ser Asp Asp Met Lys Lys Leu Lys Ala
1 5 10 15

Arg Met His Gln Ala Ile Glu Arg Phe Tyr Asp Lys Met Gln Asn Ala
20 25 30

Glu Ser Gly Arg Gly Gln Val Met Ser Ser Leu Ala Glu Leu Glu Asp
35 40 45

Asp Phe Lys Glu Gly Tyr Leu Glu Thr Val Ala Ala Tyr Tyr Glu Glu
50 55 60

Gln His Pro Glu Leu Thr Pro Leu Leu Glu Lys Glu Arg Asp Gly Leu
65 70 75 80

Arg Cys Arg Gly Asn Arg Ser Pro Val Pro Asp Val Glu Asp Pro Ala
85 90 95

Thr Glu Glu Pro Gly Glu Ser Phe Cys Asp Lys Val Met Arg Trp Phe
100 105 110

Gln Ala Met Leu Gln Arg Leu Gln Thr Trp Trp His Gly Val Leu Ala
115 120 125

Trp Val Lys Glu Lys Val Val Ala Leu Val His Ala Val Gln Ala Leu
130 135 140

Trp Lys Gln Phe Gln Ser Phe Cys Cys Ser Leu Ser Glu Leu Phe Met
145 150 155 160

Ser Ser Phe Gln Ser Tyr Gly Ala Pro Arg Gly Asp Lys Glu Glu Leu
165 170 175

Thr Pro Gln Lys Cys Ser Glu Pro Gln Ser Ser Lys
180 185

<210> 21
<211> 2254
<212> DNA
<213> Homo sapiens

<220>
<223> human Protein C inhibitor (PCI) cDNA

<220>
<221> CDS
<222> (140)..(1360)
<223> PCI

<400> 21
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agaacaaaga acagccacca tgcagctctt cctcctcttg tgcctggtgc ttctcagccc 180
tcaggggcc tcccttcacc gccaccaccc ccgggagatg aagaagagag tcgaggacct 240
ccatgtaggt gccacggtgg cccccagcag cagaagggac tttacctttg acctctacag 300

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gagcctggcc atgctctccc tgggggctgg gtccagcaca aagatgcaga tcctggaggg 420
cctgggcctc aacctccaga aaagctcaga gaaggagctg cacagaggct ttcagcagct 480
ccttcaggaa ctcaaccagc ccagagatgg cttccagctg agcctcggca atgccctttt 540
caccgacctg gtggtagacc tgcaggacac cttcgtaagt gccatgaaga cgctgtacct 600
ggcagacact ttccccacca actttaggga ctctgcaggg gccatgaagc agatcaatga 660
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tgcggtcgtg atcatggtga attacatctt ctttaaagct aagtgggaga caagcttcaa 780
ccacaaaggc acccaagagc aagacttcta cgtgacctcg gagactgtgg tgcgggtacc 840
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aaggatcaga ttcttgctgt gacccaagaa ctcctgaaat catatagaaa ggctggggtg 1980
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tagttataat ctgatgggcc tggctgggag tggaagaagg gaagcctttt gcaaatagta 2160
gagtgtcagt tgcaggtgcc aatgactaac tttttgaatt ctatgttggc attaacaata 2220
aagcattttg caaacaaaaa aaaaaaaaaa aaaa                              2254
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<210> 22
<211> 406
<212> PRT
<213> Homo sapiens

<220>
<223> human Protein C inhibitor (PCI)

<400> 22

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Met Gln Leu Phe Leu Leu Leu Cys Leu Val Leu Leu Ser Pro Gln Gly
  1               5                  10                  15

Ala Ser Leu His Arg His His Pro Arg Glu Met Lys Lys Arg Val Glu
             20                  25                  30

Asp Leu His Val Gly Ala Thr Val Ala Pro Ser Ser Arg Arg Asp Phe
         35                  40                  45

Thr Phe Asp Leu Tyr Arg Ala Leu Ala Ser Ala Ala Pro Ser Gln Asn
     50                  55                  60

Ile Phe Phe Ser Pro Val Ser Ile Ser Met Ser Leu Ala Met Leu Ser
 65                  70                  75                  80

Leu Gly Ala Gly Ser Ser Thr Lys Met Gln Ile Leu Glu Gly Leu Gly
                 85                  90                  95
```

```
Leu Asn Leu Gln Lys Ser Ser Glu Lys Glu Leu His Arg Gly Phe Gln
            100                 105                 110

Gln Leu Leu Gln Glu Leu Asn Gln Pro Arg Asp Gly Phe Gln Leu Ser
        115                 120                 125

Leu Gly Asn Ala Leu Phe Thr Asp Leu Val Val Asp Leu Gln Asp Thr
    130                 135                 140

Phe Val Ser Ala Met Lys Thr Leu Tyr Leu Ala Asp Thr Phe Pro Thr
145                 150                 155                 160

Asn Phe Arg Asp Ser Ala Gly Ala Met Lys Gln Ile Asn Asp Tyr Val
                165                 170                 175

Ala Lys Gln Thr Lys Gly Lys Ile Val Asp Leu Leu Lys Asn Leu Asp
            180                 185                 190

Ser Asn Ala Val Val Ile Met Val Asn Tyr Ile Phe Phe Lys Ala Lys
        195                 200                 205

Trp Glu Thr Ser Phe Asn His Lys Gly Thr Gln Glu Gln Asp Phe Tyr
    210                 215                 220

Val Thr Ser Glu Thr Val Val Arg Val Pro Met Met Ser Arg Glu Asp
225                 230                 235                 240

Gln Tyr His Tyr Leu Leu Asp Arg Asn Leu Ser Cys Arg Val Val Gly
                245                 250                 255

Val Pro Tyr Gln Gly Asn Ala Thr Ala Leu Phe Ile Leu Pro Ser Glu
            260                 265                 270

Gly Lys Met Gln Gln Val Glu Asn Gly Leu Ser Glu Lys Thr Leu Arg
        275                 280                 285

Lys Trp Leu Lys Met Phe Lys Lys Arg Gln Leu Glu Leu Tyr Leu Pro
    290                 295                 300

Lys Phe Ser Ile Glu Gly Ser Tyr Gln Leu Glu Lys Val Leu Pro Ser
305                 310                 315                 320

Leu Gly Ile Ser Asn Val Phe Thr Ser His Ala Asp Leu Ser Gly Ile
                325                 330                 335

Ser Asn His Ser Asn Ile Gln Val Ser Glu Met Val His Lys Ala Val
            340                 345                 350

Val Glu Val Asp Glu Ser Gly Thr Arg Ala Ala Ala Ala Thr Gly Thr
        355                 360                 365

Ile Phe Thr Phe Arg Ser Ala Arg Leu Asn Ser Gln Arg Leu Val Phe
    370                 375                 380

Asn Arg Pro Phe Leu Met Phe Ile Val Asp Asn Asn Ile Leu Phe Leu
385                 390                 395                 400

Gly Lys Val Asn Arg Pro
                405
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<210> 23
<211> 2125
<212> DNA
<213> Mus musculus

<220>
<223> mouse Protein C inhibitor (PCI), serine (or
cysteine) proteinase inhibitor, clade A, member 5
(Serpina5) cDNA

<220>
<221> CDS
<222> (125)..(1342)
<223> PCI

<400> 23
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gtgtctcacc acaaacaaag gtatcaaatc acaagcctgg ctggctgagg tggtgtggta 2040
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ctggcaataa aggcattttg caaag 2125

<210> 24
<211> 405
<212> PRT
<213> Mus musculus

<220>
<223> mouse Protein C inhibitor (PCI), serine (or cysteine) proteinase inhibitor, clade A, member 5 (Serpina5)

<400> 24

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Met Arg Phe Phe Pro Ile Leu Cys Leu Val Leu Phe Ile Ser His Gly
  1               5                  10                  15

Val Ala Ser Arg Arg His Ser His Ser Lys Lys Lys Lys Ala Lys Glu
             20                  25                  30

Ser Ser Val Gly Ala Val Gly Pro Pro Ser Ser Lys Asp Phe Ala Phe
         35                  40                  45

Arg Leu Tyr Arg Ala Leu Ala Ser Glu Ser Pro Gly Gln Asn Val Phe
     50                  55                  60

Phe Ser Pro Leu Ser Val Ser Met Ser Leu Gly Met Leu Ser Leu Gly
 65                  70                  75                  80

Ala Gly Leu Lys Thr Lys Thr Gln Ile Leu Asp Gly Leu Gly Leu Ser
                 85                  90                  95

Leu Gln Gln Gly Gln Glu Asp Lys Leu His Lys Gly Phe Gln Gln Leu
            100                 105                 110

Leu Gln Arg Phe Arg Gln Pro Ser Asp Gly Leu Gln Leu Ser Leu Gly
        115                 120                 125

Ser Ala Leu Phe Lys Asp Pro Ala Val His Ile Arg Asp Asp Phe Leu
    130                 135                 140

Ser Ala Met Lys Thr Leu Tyr Met Ser Asp Thr Phe Ser Thr Asn Phe
145                 150                 155                 160

Gly Asn Pro Glu Ile Ala Lys Lys Gln Ile Asn Asn Tyr Val Ala Lys
                165                 170                 175

Gln Thr Lys Gly Lys Ile Val Asp Leu Ile Lys Asp Leu Asp Ser Thr
            180                 185                 190

His Val Met Ile Val Val Asn Tyr Ile Phe Phe Lys Ala Lys Trp Gln
        195                 200                 205

Thr Ala Phe Ser Glu Thr Asn Thr His Lys Met Asp Phe His Val Thr
    210                 215                 220

Pro Lys Lys Thr Ile Arg Val Pro Met Met Asn Arg Glu Asp Glu Tyr
225                 230                 235                 240

Ser Tyr Tyr Leu Asp Gln Asn Ile Ser Cys Thr Val Val Gly Ile Pro
                245                 250                 255

Tyr Gln Gly Asn Ala Ile Ala Leu Phe Ile Leu Pro Ser Glu Gly Lys
            260                 265                 270

Met Lys Gln Val Glu Asp Gly Leu Asp Glu Arg Thr Leu Arg Asn Trp
        275                 280                 285
```

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Leu Lys Met Phe Thr Lys Arg Arg Leu Asp Leu Tyr Leu Pro Lys Phe
    290                 295                 300

Ser Ile Glu Ala Thr Tyr Lys Leu Glu Asn Val Leu Pro Lys Leu Gly
305                 310                 315                 320

Ile Gln Asp Val Phe Thr Thr His Ala Asp Leu Ser Gly Ile Thr Asp
                325                 330                 335

His Thr Asn Ile Lys Leu Ser Glu Met Val His Lys Ser Met Met Glu
            340                 345                 350

Val Glu Glu Ser Gly Thr Thr Ala Ala Ala Ile Thr Gly Ala Ile Phe
        355                 360                 365

Thr Phe Arg Ser Ala Arg Pro Ser Ser Leu Lys Ile Glu Phe Thr Arg
    370                 375                 380

Pro Phe Leu Leu Thr Leu Met Glu Asp Ser His Ile Leu Phe Val Gly
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Lys Val Thr Arg Pro
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<210> 25
<211> 2035
<212> DNA
<213> Rattus norvegicus

<220>
<223> rat Protein C inhibitor (PCI), serine (or cysteine) proteinase inhibitor, clade A, member 5 (Serpina5) cDNA

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<221> CDS
<222> (48)..(1268)
<223> PCI

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<210> 26
<211> 406
<212> PRT
<213> Rattus norvegicus

<220>
<223> rat Protein C inhibitor (PCI), serine (or cysteine) proteinase inhibitor, clade A, member 5 (Serpina5)

<400> 26

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Met Arg Phe Phe Pro Ile Leu Cys Leu Val Leu Phe Phe Ser His Gly
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Val Ala Ser Arg Gln Arg Ser His Ser Lys Glu Lys Lys Lys Ser Lys
             20                  25                  30

Glu Ser Ser Val Gly Ala Val Gly Thr Ser Arg Ser Arg Asp Phe Ala
         35                  40                  45

Phe Arg Leu Tyr Arg Ala Leu Ala Ser Glu Ala Pro Gly Gln Asn Val
     50                  55                  60

Phe Phe Ser Pro Met Ser Val Ser Met Ser Leu Gly Met Leu Ser Leu
 65                  70                  75                  80

Gly Ser Gly Leu Lys Thr Lys Ala Gln Ile Leu Glu Gly Leu Gly Leu
                 85                  90                  95

Ser Leu Gln Gln Gly Gln Glu Asp Met Leu His Lys Gly Phe Gln Gln
            100                 105                 110

Leu Leu Gln Gln Phe Ser Gln Pro Ser Asp Gly Leu Gln Leu Ser Leu
        115                 120                 125

Gly Ser Ala Leu Phe Thr Asp Pro Ala Val His Ile Arg Asp His Phe
    130                 135                 140

Leu Ser Ala Met Lys Thr Leu Tyr Met Ser Asp Met Phe Ser Thr Asn
145                 150                 155                 160

Phe Gly Asn Pro Glu Ser Ala Lys Lys Gln Ile Asn Asp Tyr Val Ala
                165                 170                 175
```

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Lys Lys Thr Asn Gly Lys Ile Val Asp Leu Ile Lys Asp Leu Asp Ser
            180                 185                 190

Thr His Val Met Val Val Val Asn Tyr Ile Phe Phe Lys Ala Lys Trp
        195                 200                 205

Gln Thr Ala Phe Ser Ser Thr Asn Thr His Lys Met Asp Phe His Val
    210                 215                 220

Thr Pro Lys Lys Thr Ile Gln Val Pro Met Met Asn Arg Glu Asp Ile
225                 230                 235                 240

Tyr Ser Tyr Ile Leu Asp Gln Asn Ile Ser Cys Thr Val Val Gly Ile
                245                 250                 255

Pro Tyr Gln Gly Asn Thr Phe Ala Leu Phe Ile Leu Pro Ser Glu Gly
            260                 265                 270

Lys Met Lys Arg Val Glu Asp Gly Leu Asp Glu Arg Thr Leu Arg Asn
        275                 280                 285

Trp Leu Lys Met Phe Thr Lys Arg Gln Leu Asp Leu Tyr Leu Pro Lys
    290                 295                 300

Phe Ser Ile Glu Gly Thr Tyr Lys Leu Glu Lys Ile Leu Pro Lys Leu
305                 310                 315                 320

Gly Ile Gln Asp Ile Phe Thr Thr His Ala Asp Leu Ser Gly Leu Thr
                325                 330                 335

Asp His Thr Asn Ile Lys Leu Ser Glu Met Val His Lys Ser Met Val
            340                 345                 350

Glu Val Asp Glu Ser Gly Thr Thr Ala Ala Ala Ser Thr Gly Ile Leu
        355                 360                 365

Phe Thr Leu Arg Ser Ala Arg Pro Ser Ser Leu Lys Val Glu Phe Thr
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Arg Pro Phe Leu Val Val Ile Met Asp Gly Thr Asn Leu Tyr Phe Ile
385                 390                 395                 400

Gly Lys Val Ile Gln Pro
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<210> 27
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<212> DNA
<213> Homo sapiens

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<223> human MAST205b novel variant

<220>
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<222> (1)..(5073)
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<212> PRT
<213> Homo sapiens

<220>
<223> human MAST205b novel variant

<400> 28

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Phe Ser Ala Asp Cys Ala Leu Ala Thr Ser Pro Leu Ala Ile Phe Leu
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Asn Pro Arg Ala His Ser Ser Pro Gly Thr Pro Cys Ser Ser Arg Pro
         35                  40                  45

Leu Pro Trp Ser Cys Arg Thr Ser Asn Arg Lys Ser Leu Ile Val Thr
     50                  55                  60

Ser Ser Thr Ser Pro Thr Leu Pro Arg Pro His Ser Pro Leu His Gly
 65                  70                  75                  80

His Thr Gly Asn Ser Pro Leu Asp Ser Pro Arg Asn Phe Ser Pro Asn
                 85                  90                  95

Ala Pro Ala His Phe Ser Phe Val Pro Ala Arg Ser His Ser His Arg
            100                 105                 110

Ala Asp Arg Thr Asp Gly Arg Arg Trp Ser Leu Ala Ser Leu Pro Ser
        115                 120                 125

Ser Gly Tyr Gly Thr Asn Thr Pro Ser Ser Thr Val Ser Ser Ser Cys
    130                 135                 140
```

```
Ser Ser Gln Glu Lys Leu His Gln Leu Leu Phe Gln Pro Thr Ala Asp
145                 150                 155                 160

Glu Leu His Phe Leu Thr Lys His Phe Ser Thr Glu Ser Val Pro Asp
                165                 170                 175

Glu Glu Gly Arg Gln Ser Pro Ala Met Arg Pro Arg Ser Arg Ser Leu
            180                 185                 190

Ser Pro Gly Arg Ser Pro Val Ser Phe Asp Ser Glu Ile Ile Met Met
        195                 200                 205

Asn His Val Tyr Lys Glu Arg Phe Pro Lys Ala Thr Ala Gln Met Glu
    210                 215                 220

Glu Arg Leu Ala Glu Phe Ile Ser Ser Asn Thr Pro Asp Ser Val Leu
225                 230                 235                 240

Pro Leu Ala Asp Gly Ala Leu Ser Phe Ile His His Gln Val Ile Glu
                245                 250                 255

Met Ala Arg Asp Cys Leu Asp Lys Ser Arg Ser Gly Leu Ile Thr Ser
            260                 265                 270

Gln Tyr Phe Tyr Glu Leu Gln Glu Asn Leu Glu Lys Leu Leu Gln Asp
        275                 280                 285

Ala His Glu Arg Ser Glu Ser Ser Glu Val Ala Phe Val Met Gln Leu
    290                 295                 300

Val Lys Lys Leu Met Ile Ile Ile Ala Arg Pro Ala Arg Leu Leu Glu
305                 310                 315                 320

Cys Leu Glu Phe Asp Pro Glu Glu Phe Tyr His Leu Leu Glu Ala Ala
                325                 330                 335

Glu Gly His Ala Lys Glu Gly Gln Gly Ile Lys Cys Asp Ile Pro Arg
            340                 345                 350

Tyr Ile Val Ser Gln Leu Gly Leu Thr Arg Asp Pro Leu Glu Glu Met
        355                 360                 365

Ala Gln Leu Ser Ser Cys Asp Ser Pro Asp Thr Pro Glu Thr Asp Asp
    370                 375                 380

Ser Ile Glu Gly His Gly Ala Ser Leu Pro Ser Lys Lys Thr Pro Ser
385                 390                 395                 400

Glu Glu Asp Phe Glu Thr Ile Lys Leu Ile Ser Asn Gly Ala Tyr Gly
                405                 410                 415

Ala Val Phe Leu Val Arg His Lys Ser Thr Arg Gln Arg Phe Ala Met
            420                 425                 430

Lys Lys Ile Asn Lys Gln Asn Leu Ile Leu Arg Asn Gln Ile Gln Gln
        435                 440                 445

Ala Phe Val Glu Arg Asp Ile Leu Thr Phe Ala Glu Asn Pro Phe Val
    450                 455                 460
```

Val Ser Met Phe Cys Ser Phe Asp Thr Lys Arg His Leu Cys Met Val
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Met Glu Tyr Val Glu Gly Gly Asp Cys Ala Thr Leu Leu Lys Asn Ile
485 490 495

Gly Ala Leu Pro Val Asp Met Val Arg Leu Tyr Phe Ala Glu Thr Val
500 505 510

Leu Ala Leu Glu Tyr Leu His Asn Tyr Gly Ile Val His Arg Asp Leu
515 520 525

Lys Pro Asp Asn Leu Leu Ile Thr Ser Met Gly His Ile Lys Leu Thr
530 535 540

Asp Phe Gly Leu Ser Lys Met Gly Leu Met Ser Leu Thr Thr Asn Leu
545 550 555 560

Tyr Glu Gly His Ile Glu Lys Asp Ala Arg Glu Phe Leu Asp Lys Gln
565 570 575

Val Cys Gly Thr Pro Glu Tyr Ile Ala Pro Glu Val Ile Leu Arg Gln
580 585 590

Gly Tyr Gly Lys Pro Val Asp Trp Trp Ala Met Gly Ile Ile Leu Tyr
595 600 605

Glu Phe Leu Val Gly Cys Val Pro Phe Phe Gly Asp Thr Pro Glu Glu
610 615 620

Leu Phe Gly Gln Val Ile Ser Asp Glu Ile Val Trp Pro Glu Gly Asp
625 630 635 640

Glu Ala Leu Pro Pro Asp Ala Gln Asp Leu Thr Ser Lys Leu Leu His
645 650 655

Gln Asn Pro Leu Glu Arg Leu Gly Thr Gly Ser Ala Tyr Glu Val Lys
660 665 670

Gln His Pro Phe Phe Thr Gly Leu Asp Trp Thr Gly Leu Leu Arg Gln
675 680 685

Lys Ala Glu Phe Ile Pro Gln Leu Glu Ser Glu Asp Asp Thr Ser Tyr
690 695 700

Phe Asp Thr Arg Ser Glu Arg Tyr His His Met Asp Ser Glu Asp Glu
705 710 715 720

Glu Glu Val Ser Glu Asp Gly Cys Leu Glu Ile Arg Gln Phe Ser Ser
725 730 735

Cys Ser Pro Arg Phe Asn Lys Val Tyr Ser Ser Met Glu Arg Leu Ser
740 745 750

Leu Leu Glu Glu Arg Arg Thr Pro Pro Pro Thr Lys Arg Ser Leu Ser
755 760 765

Glu Glu Lys Glu Asp His Ser Asp Gly Leu Ala Gly Leu Lys Gly Arg
770 775 780

```
Asp Arg Ser Trp Val Ile Gly Ser Pro Glu Ile Leu Arg Lys Arg Leu
785                 790                 795                 800

Ser Val Ser Glu Ser Ser His Thr Glu Ser Asp Ser Ser Pro Pro Met
                805                 810                 815

Thr Val Arg Arg Arg Cys Ser Gly Leu Leu Asp Ala Pro Arg Phe Pro
            820                 825                 830

Glu Gly Pro Glu Glu Ala Ser Ser Thr Leu Arg Arg Gln Pro Gln Glu
        835                 840                 845

Gly Ile Trp Val Leu Thr Pro Pro Ser Gly Glu Gly Val Ser Gly Pro
    850                 855                 860

Val Thr Glu His Ser Gly Glu Gln Arg Pro Lys Leu Asp Glu Glu Ala
865                 870                 875                 880

Val Gly Arg Ser Ser Gly Ser Ser Pro Ala Met Glu Thr Arg Gly Arg
                885                 890                 895

Gly Thr Ser Gln Leu Ala Glu Gly Ala Thr Ala Lys Ala Ile Ser Asp
            900                 905                 910

Leu Ala Val Arg Arg Ala Arg His Arg Leu Leu Ser Gly Asp Ser Thr
        915                 920                 925

Glu Lys Arg Thr Ala Arg Pro Val Asn Lys Val Ile Lys Ser Ala Ser
    930                 935                 940

Ala Thr Ala Leu Ser Leu Leu Ile Pro Ser Glu His His Thr Cys Ser
945                 950                 955                 960

Pro Leu Ala Ser Pro Met Ser Pro His Ser Gln Ser Ser Asn Pro Ser
                965                 970                 975

Ser Arg Asp Ser Ser Pro Ser Arg Asp Phe Leu Pro Ala Leu Gly Ser
            980                 985                 990

Met Arg Pro Pro Ile Ile Ile His Arg Ala Gly Lys Lys Tyr Gly Phe
        995                1000                1005

Thr Leu Arg Ala Ile Arg Val Tyr Met Gly Asp Ser Asp Val Tyr Thr
   1010                1015                1020

Val His His Met Val Trp His Val Glu Asp Gly Gly Pro Ala Ser Glu
1025                1030                1035                1040

Ala Gly Leu Arg Gln Gly Asp Leu Ile Thr His Val Asn Gly Glu Pro
                1045                1050                1055

Val His Gly Leu Val His Thr Glu Val Val Glu Leu Ile Leu Lys Ser
            1060                1065                1070

Gly Asn Lys Val Ala Ile Ser Thr Thr Pro Leu Glu Asn Thr Ser Ile
        1075                1080                1085

Lys Val Gly Pro Ala Arg Lys Gly Ser Tyr Lys Ala Lys Met Ala Arg
   1090                1095                1100
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Ser Ser Leu Phe Arg Lys Ile Thr Lys Gln Ala Ser Leu Leu His Thr
                1125                1130                1135

Ser Arg Ser Leu Ser Ser Leu Asn Arg Ser Leu Ser Ser Gly Glu Ser
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Gly Pro Gly Ser Pro Thr His Ser His Ser Leu Ser Pro Arg Ser Pro
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Thr Gln Gly Tyr Arg Val Thr Pro Asp Ala Val His Ser Val Gly Gly
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Asn Ser Ser Gln Ser Ser Ser Pro Ser Ser Ser Val Pro Ser Ser Pro
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Ala Gly Ser Gly His Thr Arg Pro Ser Ser Leu His Gly Leu Ala Pro
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Lys Leu Gln Arg Gln Tyr Arg Ser Pro Arg Arg Lys Ser Ala Gly Ser
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Ile Pro Leu Ser Pro Leu Ala His Thr Pro Ser Pro Pro Pro Pro Thr
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Ala Ser Pro Gln Arg Ser Pro Ser Pro Leu Ser Gly His Val Ala Gln
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Ala Phe Pro Thr Lys Leu His Leu Ser Pro Pro Leu Gly Arg Gln Leu
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Ser Arg Pro Lys Ser Ala Glu Pro Pro Arg Ser Pro Leu Leu Lys Arg
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Val Gln Ser Ala Glu Lys Leu Ala Ala Ala Leu Ala Ala Ser Glu Lys
            1300                1305                1310

Lys Leu Ala Thr Ser Arg Lys His Ser Leu Asp Leu Pro His Ser Glu
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Leu Lys Lys Glu Leu Pro Pro Arg Glu Val Ser Pro Leu Glu Val Val
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Gly Ala Arg Ser Val Leu Ser Gly Lys Gly Ala Leu Pro Gly Lys Gly
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Val Leu Gln Pro Ala Pro Ser Arg Ala Leu Gly Thr Leu Arg Gln Asp
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Arg Ala Glu Arg Arg Glu Ser Leu Gln Lys Gln Glu Ala Ile Arg Glu
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Val Asp Ser Ser Glu Asp Asp Thr Glu Glu Gly Pro Glu Asn Ser Gln
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Gly Ala Gln Glu Leu Ser Leu Ala Pro His Pro Glu Val Ser Gln Ser
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Ser Arg Gly Pro Arg Ser Leu Gly Pro Met Val Pro Ser Leu Leu Thr
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Gly Ile Thr Leu Gly Pro Pro Arg Met Glu Ser Pro Ser Gly Pro His
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Arg Arg Leu Gly Ser Pro Gln Ala Ile Glu Glu Ala Ala Ser Ser Ser
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Ser Ala Gly Pro Asn Leu Gly Gln Ser Gly Ala Thr Asp Pro Ile Pro
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Pro Glu Gly Cys Trp Lys Ala Gln His Leu His Thr Gln Ala Leu Thr
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Ala Leu Ser Pro Ser Thr Ser Gly Leu Thr Pro Thr Ser Ser Cys Ser
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Pro Pro Ser Ser Thr Ser Gly Lys Leu Ser Met Trp Ser Trp Lys Ser
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Leu Ile Glu Gly Pro Asp Arg Ala Ser Pro Ser Arg Lys Ala Thr Met
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Ala Gly Gly Leu Ala Asn Leu Gln Asp Leu Glu Asn Thr Thr Pro Ala
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Gln Pro Lys Asn Leu Ser Pro Arg Glu Gln Gly Lys Thr Gln Pro Pro
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Ser Ala Pro Arg Leu Ala His Pro Ser Tyr Glu Asp Pro Ser Gln Gly
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Trp Leu Trp Glu Ser Glu Cys Ala Gln Ala Val Lys Glu Asp Pro Ala
            1620                1625                1630

Leu Ser Ile Thr Gln Val Pro Asp Ala Ser Gly Asp Arg Arg Gln Asp
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Val Pro Cys Arg Gly Cys Pro Leu Thr Gln Lys Ser Glu Pro Ser Leu
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Pro Pro Arg Arg Arg Ala Pro Pro Gly Arg Gln Arg Leu Glu Glu Arg
         35                  40                  45
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Thr Gly Pro Ala Gly Pro Glu Gly Lys Glu Gln Asp Val Val Thr Gly
     50                  55                  60

Val Ser Pro Leu Leu Phe Arg Lys Leu Ser Asn Pro Asp Ile Phe Ser
 65                  70                  75                  80

Ser Thr Gly Lys Val Lys Leu Gln Arg Gln Leu Ser Gln Asp Asp Cys
                 85                  90                  95

Lys Leu Trp Arg Gly Asn Leu Ala Ser Ser Leu Ser Gly Lys Gln Leu
            100                 105                 110

Leu Pro Leu Ser Ser Ser Val His Ser Ser Val Gly Gln Val Thr Trp
        115                 120                 125

Gln Ser Ser Gly Glu Ala Ser Asn Leu Val Arg Met Arg Asn Gln Ser
    130                 135                 140

Leu Gly Gln Ser Ala Pro Ser Leu Thr Ala Gly Leu Lys Glu Leu Ser
145                 150                 155                 160

Leu Pro Arg Arg Gly Ser Phe Cys Arg Thr Ser Asn Arg Lys Ser Leu
                165                 170                 175

Ile Val Thr Ser Ser Thr Ser Pro Thr Leu Pro Arg Pro His Ser Pro
            180                 185                 190

Leu His Gly His Thr Gly Asn Ser Pro Leu Asp Ser Pro Arg Asn Phe
        195                 200                 205

Ser Pro Asn Ala Pro Ala His Phe Ser Phe Val Pro Ala Arg Arg Thr
    210                 215                 220

Asp Gly Arg Arg Trp Ser Leu Ala Ser Leu Pro Ser Ser Gly Tyr Gly
225                 230                 235                 240

Thr Asn Thr Pro Ser Ser Thr Val Ser Ser Ser Cys Ser Ser Gln Glu
                245                 250                 255

Lys Leu His Gln Leu Pro Phe Gln Pro Thr Ala Asp Glu Leu His Phe
            260                 265                 270

Leu Thr Lys His Phe Ser Thr Glu Ser Val Pro Asp Glu Glu Gly Arg
        275                 280                 285

Gln Ser Pro Ala Met Arg Pro Arg Ser Arg Ser Leu Ser Pro Gly Arg
    290                 295                 300

Ser Pro Val Ser Phe Asp Ser Glu Ile Ile Met Met Asn His Val Tyr
305                 310                 315                 320

Lys Glu Arg Phe Pro Lys Ala Thr Ala Gln Met Glu Glu Arg Leu Ala
                325                 330                 335

Glu Phe Ile Ser Ser Asn Thr Pro Asp Ser Val Leu Pro Leu Ala Asp
            340                 345                 350

Gly Ala Leu Ser Phe Ile His His Gln Val Ile Glu Met Ala Arg Asp
        355                 360                 365
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Cys Leu Asp Lys Ser Arg Ser Gly Leu Ile Thr Ser Gln Tyr Phe Tyr
    370                 375                 380

Glu Leu Gln Glu Asn Leu Glu Lys Leu Leu Gln Asp Ala His Glu Arg
385                 390                 395                 400

Ser Glu Ser Ser Glu Val Ala Phe Val Met Gln Leu Val Lys Lys Leu
                405                 410                 415

Met Ile Ile Ile Ala Arg Pro Ala Arg Leu Leu Glu Cys Leu Glu Phe
            420                 425                 430

Asp Pro Glu Glu Phe Tyr His Leu Leu Glu Ala Ala Glu Gly His Ala
        435                 440                 445

Lys Glu Gly Gln Gly Ile Lys Cys Asp Ile Pro Arg Tyr Ile Val Ser
    450                 455                 460

Gln Leu Gly Leu Thr Arg Asp Pro Leu Glu Glu Met Ala Gln Leu Ser
465                 470                 475                 480

Ser Cys Asp Ser Pro Asp Thr Pro Glu Thr Asp Asp Ser Ile Glu Gly
                485                 490                 495

His Gly Ala Ser Leu Pro Ser Lys Lys Thr Pro Ser Glu Glu Asp Phe
            500                 505                 510

Glu Thr Ile Lys Leu Ile Ser Asn Gly Ala Tyr Gly Ala Val Phe Leu
        515                 520                 525

Val Arg His Lys Ser Thr Arg Gln Arg Phe Ala Met Lys Lys Ile Asn
    530                 535                 540

Lys Gln Asn Leu Ile Leu Arg Asn Gln Ile Gln Gln Ala Phe Val Glu
545                 550                 555                 560

Arg Asp Ile Leu Thr Phe Ala Glu Asn Pro Phe Val Val Ser Met Phe
                565                 570                 575

Cys Ser Phe Asp Thr Lys Arg His Leu Cys Met Val Met Glu Tyr Val
            580                 585                 590

Glu Gly Gly Asp Cys Ala Thr Leu Leu Lys Asn Ile Gly Ala Leu Pro
        595                 600                 605

Val Asp Met Val Arg Leu Tyr Phe Ala Glu Thr Val Leu Ala Leu Glu
    610                 615                 620

Tyr Leu His Asn Tyr Gly Ile Val His Arg Asp Leu Lys Pro Asp Asn
625                 630                 635                 640

Leu Leu Ile Thr Ser Met Gly His Ile Lys Leu Thr Asp Phe Gly Leu
                645                 650                 655

Ser Lys Met Gly Leu Met Ser Leu Thr Thr Asn Leu Tyr Glu Gly His
            660                 665                 670

Ile Glu Lys Asp Ala Arg Glu Phe Leu Asp Lys Gln Val Cys Gly Thr
        675                 680                 685
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Pro Glu Tyr Ile Ala Pro Glu Val Ile Leu Arg Gln Gly Tyr Gly Lys
    690                 695                 700

Pro Val Asp Trp Trp Ala Met Gly Ile Ile Leu Tyr Glu Phe Leu Val
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Gly Cys Val Pro Phe Phe Gly Asp Thr Pro Glu Glu Leu Phe Gly Gln
                725                 730                 735

Val Ile Ser Asp Glu Ile Val Trp Pro Glu Gly Asp Glu Ala Leu Pro
            740                 745                 750

Pro Asp Ala Gln Asp Leu Thr Ser Lys Leu Leu His Gln Asn Pro Leu
        755                 760                 765

Glu Arg Leu Gly Thr Gly Ser Ala Tyr Glu Val Lys Gln His Pro Phe
    770                 775                 780

Phe Thr Gly Leu Asp Trp Thr Gly Leu Leu Arg Gln Lys Ala Glu Phe
785                 790                 795                 800

Ile Pro Gln Leu Glu Ser Glu Asp Asp Thr Ser Tyr Phe Asp Thr Arg
                805                 810                 815

Ser Glu Arg Tyr His His Met Asp Ser Glu Asp Glu Glu Glu Val Ser
            820                 825                 830

Glu Asp Gly Cys Leu Glu Ile Arg Gln Phe Ser Ser Cys Ser Pro Arg
        835                 840                 845

Phe Asn Lys Val Tyr Ser Ser Met Glu Arg Leu Ser Leu Leu Glu Glu
    850                 855                 860

Arg Arg Thr Pro Pro Pro Thr Lys Arg Ser Leu Ser Glu Glu Lys Glu
865                 870                 875                 880

Asp His Ser Asp Gly Leu Ala Gly Leu Lys Gly Arg Asp Arg Ser Trp
                885                 890                 895

Val Ile Gly Ser Pro Glu Ile Leu Arg Lys Arg Leu Ser Val Ser Glu
            900                 905                 910

Ser Ser His Thr Glu Ser Asp Ser Ser Pro Pro Met Thr Val Arg Arg
        915                 920                 925

Arg Cys Ser Gly Leu Leu Asp Ala Pro Arg Phe Pro Glu Gly Pro Glu
    930                 935                 940

Glu Ala Ser Ser Thr Leu Arg Arg Gln Pro Gln Glu Gly Ile Trp Val
945                 950                 955                 960

Leu Thr Pro Pro Ser Gly Glu Gly Val Ser Gly Pro Val Thr Glu His
                965                 970                 975

Ser Gly Glu Gln Arg Pro Lys Leu Asp Glu Glu Ala Val Gly Arg Ser
            980                 985                 990

Ser Gly Ser Ser Pro Ala Met Glu Thr Arg Gly Arg Gly Thr Ser Gln
        995                1000                1005
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Arg Ala Arg His Arg Leu Leu Ser Gly Asp Ser Thr Glu Lys Arg Thr
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Ala Arg Pro Val Asn Lys Val Ile Lys Ser Ala Ser Ala Thr Ala Leu
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Ser Leu Leu Ile Pro Ser Glu His His Thr Cys Ser Pro Leu Ala Ser
           1060                1065                1070

Pro Met Ser Pro His Ser Gln Ser Ser Asn Pro Ser Ser Arg Asp Ser
       1075                1080                1085

Ser Pro Ser Arg Asp Phe Leu Pro Ala Leu Gly Ser Met Arg Pro Pro
   1090                1095                1100

Ile Ile Ile His Arg Ala Gly Lys Lys Tyr Gly Phe Thr Leu Arg Ala
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Ile Arg Val Tyr Met Gly Asp Ser Asp Val Tyr Thr Val His His Met
               1125                1130                1135

Val Trp His Val Glu Asp Gly Gly Pro Ala Ser Glu Ala Gly Leu Arg
           1140                1145                1150

Gln Gly Asp Leu Ile Thr His Val Asn Gly Glu Pro Val His Gly Leu
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Val His Thr Glu Val Val Glu Leu Ile Leu Lys Ser Gly Asn Lys Val
   1170                1175                1180

Ala Ile Ser Thr Thr Pro Leu Glu Asn Thr Ser Ile Lys Val Gly Pro
1185                1190                1195                1200

Ala Arg Lys Gly Ser Tyr Lys Ala Lys Met Ala Arg Arg Ser Lys Arg
               1205                1210                1215

Ser Arg Gly Lys Asp Gly Gln Glu Ser Arg Lys Arg Ser Ser Leu Phe
           1220                1225                1230

Arg Lys Ile Thr Lys Gln Ala Ser Leu Leu His Thr Ser Arg Ser Leu
       1235                1240                1245

Ser Ser Leu Asn Arg Ser Leu Ser Ser Gly Glu Ser Gly Pro Gly Ser
   1250                1255                1260

Pro Thr His Ser His Ser Leu Ser Pro Arg Ser Pro Thr Gln Gly Tyr
1265                1270                1275                1280

Arg Val Thr Pro Asp Ala Val His Ser Val Gly Gly Asn Ser Ser Gln
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Ser Ser Ser Pro Ser Ser Ser Val Pro Ser Ser Pro Ala Gly Ser Gly
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His Thr Arg Pro Ser Ser Leu His Gly Leu Ala Pro Lys Leu Gln Arg
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Gln Tyr Arg Ser Pro Arg Arg Lys Ser Ala Gly Ser Ile Pro Leu Ser
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Pro Leu Ala His Thr Pro Ser Pro Pro Pro Pro Thr Ala Ser Pro Gln
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Arg Ser Pro Ser Pro Leu Ser Gly His Val Ala Gln Ala Phe Pro Thr
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Lys Leu His Leu Ser Pro Pro Leu Gly Arg Gln Leu Ser Arg Pro Lys
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Ser Ala Glu Pro Pro Arg Ser Pro Leu Leu Lys Arg Val Gln Ser Ala
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Glu Lys Leu Ala Ala Ala Leu Ala Ala Ser Glu Lys Lys Leu Ala Thr
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Ser Arg Lys His Ser Leu Asp Leu Pro His Ser Glu Leu Lys Lys Glu
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Leu Pro Pro Arg Glu Val Ser Pro Leu Glu Val Val Gly Ala Arg Ser
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Val Leu Ser Gly Lys Gly Ala Leu Pro Gly Lys Gly Val Leu Gln Pro
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Ala Pro Ser Arg Ala Leu Gly Thr Leu Arg Gln Asp Arg Ala Glu Arg
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Arg Glu Ser Leu Gln Lys Gln Glu Ala Ile Arg Glu Val Asp Ser Ser
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Glu Asp Asp Thr Glu Glu Gly Pro Glu Asn Ser Gln Gly Ala Gln Glu
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Leu Ser Leu Ala Pro His Pro Glu Val Ser Gln Ser Val Ala Pro Lys
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Gly Ala Gly Glu Ser Gly Glu Glu Asp Pro Phe Pro Ser Arg Gly Pro
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Arg Ser Leu Gly Pro Met Val Pro Ser Leu Leu Thr Gly Ile Thr Leu
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Gly Pro Pro Arg Met Glu Ser Pro Ser Gly Pro His Arg Arg Leu Gly
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Ser Pro Gln Ala Ile Glu Glu Ala Ala Ser Ser Ser Ser Ala Gly Pro
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Asn Leu Gly Gln Ser Gly Ala Thr Asp Pro Ile Pro Pro Glu Gly Cys
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Trp Lys Ala Gln His Leu His Thr Gln Ala Leu Thr Ala Leu Ser Pro
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Ser Thr Ser Gly Leu Thr Pro Thr Ser Ser Cys Ser Pro Pro Ser Ser
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Thr Ser Gly Lys Leu Ser Met Trp Ser Trp Lys Ser Leu Ile Glu Gly
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Ala Asn Leu Gln Asp Leu Glu Thr Gln Leu Gln Pro Ser Leu Arg Thr
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Cys Leu Pro Gly Ser Arg Gly Arg His Ser His Leu Val Pro Pro Asp
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Trp Pro Ile His Leu Met Arg Ile Pro Ala Arg Ala Gly Tyr Gly Ser
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Leu Ser Val His Lys Gln
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Lys Glu Leu Ser Leu Pro Arg Arg Gly Ser Phe Cys Arg Thr Ser Asn
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Ala Arg Arg Thr Asp Gly Arg Arg Trp Ser Leu Ala Ser Leu Pro Ser
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Ser Gly Tyr Gly Thr Asn Thr Pro Ser Ser Thr Val Ser Ser Ser Cys
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Leu Pro Leu Ala Asp Gly Ala Leu Ser Phe Ile His His Gln Val Ile
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Glu Met Ala Arg Asp Cys Leu Asp Lys Ser Arg Ser Gly Leu Ile Thr
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Ser His Tyr Phe Tyr Glu Leu Gln Glu Asn Leu Glu Lys Leu Leu Gln
                325                 330                 335

Asp Ala His Glu Arg Ser Glu Ser Ser Asp Val Ala Phe Val Ile Gln
            340                 345                 350

Leu Val Lys Lys Leu Met Ile Ile Ile Ala Arg Pro Ala Arg Leu Leu
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Glu Cys Leu Glu Phe Asp Pro Glu Glu Phe Tyr His Leu Leu Glu Ala
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Ala Glu Gly His Ala Lys Glu Gly His Gly Ile Lys Cys Asp Ile Pro
385                 390                 395                 400

Arg Tyr Ile Val Ser Gln Leu Gly Leu Thr Arg Asp Pro Leu Glu Glu
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Met Ala Gln Leu Ser Ser Tyr Asp Ser Pro Asp Thr Pro Glu Thr Asp
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Asp Ser Val Glu Gly Arg Gly Val Ser Gln Pro Ser Gln Lys Thr Pro
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Ser Glu Glu Asp Phe Glu Thr Ile Lys Leu Ile Ser Asn Gly Ala Tyr
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Gly Ala Val Phe Leu Val Arg His Lys Ser Thr Arg Gln Arg Phe Ala
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Met Lys Lys Ile Asn Lys Gln Asn Leu Ile Leu Arg Asn Gln Ile Gln
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Gln Ala Phe Val Glu Arg Asp Ile Leu Thr Phe Ala Glu Asn Pro Phe
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Val Val Ser Met Phe Cys Ser Phe Glu Thr Lys Arg His Leu Cys Met
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Val Met Glu Tyr Val Glu Gly Gly Asp Cys Ala Thr Leu Leu Lys Asn
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Ile Gly Ala Leu Pro Val Asp Met Val Arg Leu Tyr Phe Ala Glu Thr
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Thr Asp Phe Gly Leu Ser Lys Ile Gly Leu Met Ser Leu Thr Thr Asn
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Leu Tyr Glu Gly His Ile Glu Lys Asp Ala Arg Glu Phe Leu Asp Lys
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Gln Val Cys Gly Thr Pro Glu Tyr Ile Ala Pro Glu Val Ile Leu Arg
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Gln Gly Tyr Gly Lys Pro Val Asp Trp Trp Ala Met Gly Ile Ile Leu
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Tyr Glu Phe Leu Val Gly Cys Val Pro Phe Phe Gly Asp Thr Pro Glu
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Glu Leu Phe Gly Gln Val Ile Ser Asp Glu Ile Val Trp Pro Glu Gly
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Asp Asp Ala Leu Pro Pro Asp Ala Gln Asp Leu Thr Ser Lys Leu Leu
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His Gln Asn Pro Leu Glu Arg Leu Gly Thr Ser Ser Ala Tyr Glu Val
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Lys Gln His Pro Phe Phe Met Gly Leu Asp Trp Thr Gly Leu Leu Arg
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Gln Lys Ala Glu Phe Ile Pro Gln Leu Glu Ser Glu Asp Asp Thr Ser
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Tyr Phe Asp Thr Arg Ser Glu Arg Tyr His His Val Asp Ser Glu Asp
755 760 765

Glu Glu Glu Val Ser Glu Asp Gly Cys Leu Glu Ile Arg Gln Phe Ser
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Ser Cys Ser Pro Arg Phe Ser Lys Val Tyr Ser Ser Met Glu Arg Leu
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Arg Asp Arg Ser Trp Val Ile Gly Ser Pro Glu Ile Leu Arg Lys Arg
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Leu Ser Val Ser Glu Ser Ser His Thr Glu Ser Asp Ser Ser Pro Pro
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Met Thr Val Arg His Arg Cys Ser Gly Leu Pro Asp Gly Pro His Cys
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Glu Arg Pro Leu Glu Arg Gln Leu Lys Leu Asp Glu Glu Pro Pro Gly
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Gln Ser Ser Arg Cys Cys Pro Ala Leu Glu Thr Arg Gly Arg Gly Thr
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Pro Gln Leu Ala Glu Glu Ala Thr Ala Lys Ala Ile Ser Asp Leu Ala
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Val Arg Arg Ala Arg His Arg Leu Leu Ser Gly Asp Ser Ile Glu Lys
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Arg Thr Thr Arg Pro Val Asn Lys Val Ile Lys Ser Ala Ser Ala Thr
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Asp Ser Ser Pro Ser Arg Asp Phe Leu Pro Ala Leu Gly Ser Leu Arg
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Pro Pro Ile Ile Ile His Arg Ala Gly Lys Lys Tyr Gly Phe Thr Leu
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Arg Ala Ile Arg Val Tyr Met Gly Asp Thr Asp Val Tyr Thr Val His
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His Met Val Trp His Val Glu Asp Gly Gly Pro Ala Ser Glu Ala Gly
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Leu Arg Gln Gly Asp Leu Ile Thr His Val Asn Gly Glu Pro Val His
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Gly Leu Val His Thr Glu Val Val Glu Leu Val Leu Lys Ser Gly Asn
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Lys Val Ser Ile Ser Thr Thr Pro Leu Glu Asn Thr Ser Ile Lys Val
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Gly Pro Ala Arg Lys Gly Ser Tyr Lys Ala Lys Met Ala Arg Arg Ser
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Lys Arg Ser Lys Gly Lys Asp Gly Gln Glu Ser Arg Lys Arg Ser Ser
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Leu Phe Arg Lys Ile Thr Lys Gln Ala Ser Leu Leu His Thr Ser Arg
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Ser Gly His Thr Arg Pro Ser Ser Leu His Gly Leu Ala Pro Lys Leu
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Gln Arg Gln Tyr Arg Ser Pro Arg Arg Lys Ser Ala Gly Ser Ile Pro
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Pro Gln Arg Ser Pro Ser Pro Leu Ser Gly His Gly Ser Gln Ser Phe
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Pro Thr Lys Leu His Leu Ser Pro Pro Leu Gly Arg Gln Leu Ser Arg
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Pro Lys Ser Ala Glu Pro Pro Arg Ser Pro Leu Leu Lys Arg Val Gln
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Ser Ala Glu Lys Leu Ala Ala Ala Leu Ala Ala Ala Glu Lys Lys Leu
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Ala Pro Ser Arg Lys His Ser Leu Asp Leu Pro His Gly Glu Leu Lys
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Lys Glu Leu Thr Pro Arg Glu Ala Ser Pro Leu Glu Val Val Gly Thr
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Arg Ser Val Leu Ser Gly Lys Gly Pro Leu Pro Gly Lys Gly Val Leu
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Gln Pro Ala Pro Ser Arg Ala Leu Gly Thr Leu Arg Gln Asp Arg Ala
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Glu Arg Arg Glu Ser Leu Gln Lys Gln Glu Ala Ile Arg Glu Val Asp
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Pro Lys Gly Ser Gly Glu Gly Thr Glu Glu Asp Thr Phe Leu His Arg
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Asp Leu Lys Lys Gln Gly Pro Val Leu Ser Gly Leu Val Thr Gly Ala
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Pro Asp Arg Ala Ser Thr Asn Lys Thr Ile Thr Arg Lys Gly Glu Pro
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Ala Asn Ser Gln Asp Thr Asn Thr Thr Val Pro Asn Leu Leu Lys Asn
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Leu Ser Pro Glu Glu Glu Lys Pro Gln Pro Pro Ser Val Pro Gly Leu
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Thr His Pro Leu Leu Glu Val Pro Ser Gln Asn Trp Pro Trp Glu Ser
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Glu Cys Glu Gln Met Glu Lys Glu Glu Pro Ser Leu Ser Ile Thr Glu
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His Pro Leu Ser Pro Glu Thr Arg Pro Ser Leu Leu Trp Lys Ser Gln
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cagaagaaga atggattgta tgtcaagatt ttacttggca ttgagtagtt tttttcaata 2340
gtaggtaatt ccttagagat acagtatacc tggcaattca caaatagcca ttgaacaaat 2400
gtgtgggttt ttaaaaatta tatactatat gagttgccta tatttgctat tcaaaatttt 2460
gtaaatatgc aaatcagctt tataggttta ttacaagttt tttaggattc ttttggggaa 2520
gagtcataat tcttttgaaa ataaccatga atacacttac agttaggatt tgtggtaagg 2580
tacctctcaa cattaccaaa atcatttctt tagagggaag gaataatcat tcaaatgaac 2640
tttaaaaaag caaatttcat gcactgatta aaataggatt attttaaata caaaaggcat 2700
tttatatgaa ttataaactg aagagcttaa agatagttac aaatacaaaa gttcaacctc 2760
ttacaataag ctaaacgcaa tgtcttttta aaaagaggac ttagggtgtc gtttttcaca 2820
tatgacaatg ttgcatttat gatgcagttt caagtaccaa aacgttgaat tgatgatgca 2880
gttttcatat atcgagatgt tcgctcgtgc agtactgttg gttaaatgac aatttatgtg 2940
gattttgcat gtaatacaca gtgagacaca gtaattttat ctaaattaca gtgcagttta 3000
gttaatctat taatactgac tcagtgtctg cctttaaata taaatgatat gttgaaaact 3060
taaggaagca aatgctacat atatgcaata taaaatagta atgtgatgct gatgctgtta 3120
accaaagggc agaataaata agcaaaatgc caaaaggggt cttaattgaa atgaaaattt 3180
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tagaagacaa ttttcataac ttgataaatt atagttttgt ttgttagaaa agtagctctt 3300
aaaagatgta aatagatgac aaacgatgta aataattttg taagaggctt caaaatgttt 3360
atacgtggaa acacacctac atgaaaagca gaaatcggtt gctgttttgc ttctttttcc 3420
ctcttatttt tgtattgtgg tcatttccta tgcaaataat ggagcaaaca gctgtatagt 3480
tgtagaattt tttgagagaa tgagatgttt atatattaac gacaattttt ttttggaaaa 3540
taaaaagtgc cctaaaagaa aaaaaaaa 3568

<210> 34
<211> 457
<212> PRT
<213> Homo sapiens

<220>
<223> human colon Kruppel-like factor (CKLF)

<400> 34
Met Ala Thr Arg Val Leu Ser Met Ser Ala Arg Leu Gly Pro Val Pro
1 5 10 15

Gln Pro Pro Ala Pro Gln Asp Glu Pro Val Phe Ala Gln Leu Lys Pro
20 25 30

Val Leu Gly Ala Ala Asn Pro Ala Arg Asp Ala Ala Leu Phe Pro Gly
35 40 45

Glu Glu Leu Lys His Ala His His Arg Pro Gln Ala Gln Pro Ala Pro
50 55 60

Ala Gln Ala Pro Gln Pro Ala Gln Pro Pro Ala Thr Gly Pro Arg Leu
65 70 75 80

Pro Pro Glu Asp Leu Val Gln Thr Arg Cys Glu Met Glu Lys Tyr Leu
85 90 95

Thr Pro Gln Leu Pro Pro Val Pro Ile Ile Pro Glu His Lys Lys Tyr
100 105 110

Arg Arg Asp Ser Ala Ser Val Val Asp Gln Phe Phe Thr Asp Thr Glu
115 120 125

Gly Leu Pro Tyr Ser Ile Asn Met Asn Val Phe Leu Pro Asp Ile Thr
130 135 140

His Leu Arg Thr Gly Leu Tyr Lys Ser Gln Arg Pro Cys Val Thr His
145 150 155 160

Ile Lys Thr Glu Pro Val Ala Ile Phe Ser His Gln Ser Glu Thr Thr
165 170 175

Ala Pro Pro Pro Ala Pro Thr Gln Ala Leu Pro Glu Phe Thr Ser Ile
180 185 190

Phe Ser Ser His Gln Thr Ala Ala Pro Glu Val Asn Asn Ile Phe Ile
195 200 205

Lys Gln Glu Leu Pro Thr Pro Asp Leu His Leu Ser Val Pro Thr Gln
210 215 220

Gln Gly His Leu Tyr Gln Leu Leu Asn Thr Pro Asp Leu Asp Met Pro
225 230 235 240

Ser Ser Thr Asn Gln Thr Ala Ala Met Asp Thr Leu Asn Val Ser Met
245 250 255

Ser Ala Ala Met Ala Gly Leu Asn Thr His Thr Ser Ala Val Pro Gln
260 265 270

```
Thr Ala Val Lys Gln Phe Gln Gly Met Pro Pro Cys Thr Tyr Thr Met
        275                 280                 285

Pro Ser Gln Phe Leu Pro Gln Gln Ala Thr Tyr Phe Pro Pro Ser Pro
    290                 295                 300

Pro Ser Ser Glu Pro Gly Ser Pro Asp Arg Gln Ala Glu Met Leu Gln
305                 310                 315                 320

Asn Leu Thr Pro Pro Pro Ser Tyr Ala Ala Thr Ile Ala Ser Lys Leu
                325                 330                 335

Ala Ile His Asn Pro Asn Leu Pro Thr Thr Leu Pro Val Asn Ser Gln
            340                 345                 350

Asn Ile Gln Pro Val Arg Tyr Asn Arg Arg Ser Asn Pro Asp Leu Glu
        355                 360                 365

Lys Arg Arg Ile His Tyr Cys Asp Tyr Pro Gly Cys Thr Lys Val Tyr
    370                 375                 380

Thr Lys Ser Ser His Leu Lys Ala His Leu Arg Thr His Thr Gly Glu
385                 390                 395                 400

Lys Pro Tyr Lys Cys Thr Trp Glu Gly Cys Asp Trp Arg Phe Ala Arg
                405                 410                 415

Ser Asp Glu Leu Thr Arg His Tyr Arg Lys His Thr Gly Ala Lys Pro
            420                 425                 430

Phe Gln Cys Gly Val Cys Asn Arg Ser Phe Ser Arg Ser Asp His Leu
        435                 440                 445

Ala Leu His Met Lys Arg His Gln Asn
    450                 455
```

<210> 35
<211> 1591
<212> DNA
<213> Mus musculus

<220>
<223> mouse intestinal-enriched Kruppel-like factor
(IKLF, CKLF) cDNA

<220>
<221> CDS
<222> (167)..(1507)
<223> CKLF

<400> 35
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gggtcccccg ccgcggcccc ccgccgagtc cgccgtcccg tgccagcccg agcgaggtgg 120
gatcgcgatc gctccgtgtc ccgctcccgt aatccccaga ccgtccatgc ccacgcgggt 180
gctgaccatg agcgcccgcc tgggaccact gccccagccg ccggccgcgc aggccgagcc 240
cgtgttcgcg cagctcaagc cggtgctggg cgctgcgaac ccggcccgcg acgcggcgct 300
cttctccgga gacgatctga aacacgcgca ccaccacccg cctgcgccgc cgccagccgc 360
tggcccgcga ctgccctcgg aggagctggt ccagacaaga tgtgaaatgg agaagtatct 420
gacccctcag ctccctccag ttccgataat ttcagagcat aaaaagtata gacgagacag 480
tgcctcagtg gtagaccagt tcttcactga cactgaaggc ataccttaca gcatcaacat 540
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```
gaacgtcttc ctccctgaca tcactcacct gagaactggc ctctacaaat cccagagacc 600
atgcgtaaca cagatcaaga cagaacctgt taccattttc agccaccaga gcgagtcgac 660
ggcccctcct cctcctccgg cccccaccca ggctctcccc gagttcacta gtatcttcag 720
ctcccaccag accacagcgc caccacagga ggtgaacaat atcttcatca aacaagaact 780
tcctatacca gatcttcatc tctctgtccc ttcccagcag ggccacctgt accagctgtt 840
gaatacaccg gatctagaca tgcccagttc gacaaaccag acggcagtaa tggacaccct 900
taatgtttct atggcaggcc ttaacccaca cccctctgct gttccacaga cgtcaatgaa 960
acagttccag ggcatgcccc cttgcacgta caccatgcca agtcagtttc ttccacagca 1020
ggccacttat tttcccccgt caccaccaag ctcagagcct ggaagtcccg atagacaagc 1080
tgagatgctg cagaatctca ccccacctcc gtcctatgcc gctacaattg cttccaaact 1140
ggcgattcac aacccaaatt tacctgccac tctgccagtt aattcgccaa ctctcccacc 1200
tgtcagatac aacagaagga gtaacccgga tctggagaag cgacgtatcc acttctgcga 1260
ttataatggt tgcacaaaag tttatacaaa gtcgtctcac ttaaaagctc acctgaggac 1320
tcatacgggc gagaagccct acaagtgcac ctgggagggc tgcgactgga ggtttgcccg 1380
gtcggatgag ctgacccgcc actacaggaa gcacacgggc gccaagccgt tccagtgcat 1440
ggtgtgccaa cgcagcttct cccgctccga ccacctcgcg ctgcacatga agcgccacca 1500
gaactgagcg agcgaacgct gcgcccaccc gcctgacgcc ttgcagtccg ctttgccatc 1560
ctttaaaccg cagacctaac ttcataaaaa g                                1591
```

<210> 36
<211> 446
<212> PRT
<213> Mus musculus

<220>
<223> mouse intestinal-enriched Kruppel-like factor
(IKLF, CKLF)

<400> 36

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Met Pro Thr Arg Val Leu Thr Met Ser Ala Arg Leu Gly Pro Leu Pro
  1               5                  10                  15

Gln Pro Pro Ala Ala Gln Ala Glu Pro Val Phe Ala Gln Leu Lys Pro
             20                  25                  30

Val Leu Gly Ala Ala Asn Pro Ala Arg Asp Ala Ala Leu Phe Ser Gly
         35                  40                  45

Asp Asp Leu Lys His Ala His His His Pro Pro Ala Pro Pro Pro Ala
     50                  55                  60

Ala Gly Pro Arg Leu Pro Ser Glu Glu Leu Val Gln Thr Arg Cys Glu
 65                  70                  75                  80

Met Glu Lys Tyr Leu Thr Pro Gln Leu Pro Pro Val Pro Ile Ile Ser
                 85                  90                  95

Glu His Lys Lys Tyr Arg Arg Asp Ser Ala Ser Val Val Asp Gln Phe
            100                 105                 110

Phe Thr Asp Thr Glu Gly Ile Pro Tyr Ser Ile Asn Met Asn Val Phe
        115                 120                 125

Leu Pro Asp Ile Thr His Leu Arg Thr Gly Leu Tyr Lys Ser Gln Arg
    130                 135                 140

Pro Cys Val Thr Gln Ile Lys Thr Glu Pro Val Thr Ile Phe Ser His
145                 150                 155                 160
```

```
Gln Ser Glu Ser Thr Ala Pro Pro Pro Pro Pro Ala Pro Thr Gln Ala
                165                 170                 175

Leu Pro Glu Phe Thr Ser Ile Phe Ser Ser His Gln Thr Thr Ala Pro
            180                 185                 190

Pro Gln Glu Val Asn Asn Ile Phe Ile Lys Gln Glu Leu Pro Ile Pro
        195                 200                 205

Asp Leu His Leu Ser Val Pro Ser Gln Gln Gly His Leu Tyr Gln Leu
    210                 215                 220

Leu Asn Thr Pro Asp Leu Asp Met Pro Ser Ser Thr Asn Gln Thr Ala
225                 230                 235                 240

Val Met Asp Thr Leu Asn Val Ser Met Ala Gly Leu Asn Pro His Pro
                245                 250                 255

Ser Ala Val Pro Gln Thr Ser Met Lys Gln Phe Gln Gly Met Pro Pro
            260                 265                 270

Cys Thr Tyr Thr Met Pro Ser Gln Phe Leu Pro Gln Gln Ala Thr Tyr
        275                 280                 285

Phe Pro Pro Ser Pro Pro Ser Ser Glu Pro Gly Ser Pro Asp Arg Gln
    290                 295                 300

Ala Glu Met Leu Gln Asn Leu Thr Pro Pro Pro Ser Tyr Ala Ala Thr
305                 310                 315                 320

Ile Ala Ser Lys Leu Ala Ile His Asn Pro Asn Leu Pro Ala Thr Leu
                325                 330                 335

Pro Val Asn Ser Pro Thr Leu Pro Pro Val Arg Tyr Asn Arg Arg Ser
            340                 345                 350

Asn Pro Asp Leu Glu Lys Arg Arg Ile His Phe Cys Asp Tyr Asn Gly
        355                 360                 365

Cys Thr Lys Val Tyr Thr Lys Ser Ser His Leu Lys Ala His Leu Arg
    370                 375                 380

Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Thr Trp Glu Gly Cys Asp
385                 390                 395                 400

Trp Arg Phe Ala Arg Ser Asp Glu Leu Thr Arg His Tyr Arg Lys His
                405                 410                 415

Thr Gly Ala Lys Pro Phe Gln Cys Met Val Cys Gln Arg Ser Phe Ser
            420                 425                 430

Arg Ser Asp His Leu Ala Leu His Met Lys Arg His Gln Asn
        435                 440                 445
```

<210> 37
<211> 877
<212> DNA
<213> Rattus norvegicus

<220>
<223> rat Kruppel-like factor 5, intestinal (KLF5, CKLF)
cDNA

<220>
<221> CDS
<222> (145)..(792)
<223> CKLF

<400> 37
cggtatttca gctcccacca gaccacagcg ccagaggtga acaatatctt catcaaacaa 60
gaacttccta taccagatct tcatctctcg gtcccttccc agcagggcca cctgtaccag 120
ctgttgaata cacctgatct agacatgccc agttcgacaa accagacagc agtcatggac 180
acccttaatg tctctatggc tggccttaac tcacacccct ctgctgtgcc acagacgtcc 240
atgaaacagt tccagggcat gcctccttgc acgtacacca tgccgagtca gtttcttcca 300
cagcaggcca cctactttcc cccatcacca ccgagctcag agcctggaag tcctgataga 360
caagctgaga tgctccagaa tctgacccca cctccgtcct atgctgctac aattgcttcg 420
aaactggcaa ttcacaatcc aaatttacct gccactctgc cagttaattc gccaaatatc 480
caacctgtcc gatacaacag aaggagtaac ccggatctgg agaagcgacg catccatttc 540
tgtgattatg atggttgcac aaaagtttat acaaagtcgt ctcatttaaa agctcacctg 600
aggactcata cgggcgagaa gccctacaag tgcacctggg agggctgcga ctggaggttt 660
gcccggtcgg acgagctgac ccgccactac aggaagcaca cgggtgccaa gccgttccag 720
tgcgtggtgt gcaaccgcag cttctcccgc tccgaccacc tggcgctgca catgaagcgc 780
caccagaact gagcactgcg cacaaccggc tcgacgcctc gcagtccgct cgccatcctt 840
taaaccgcag acctaacttc atataaaaaa aaaaaaa 877

<210> 38
<211> 215
<212> PRT
<213> Rattus norvegicus

<220>
<223> rat Kruppel-like factor 5, intestinal (KLF5, CKLF)

<400> 38
Met Pro Ser Ser Thr Asn Gln Thr Ala Val Met Asp Thr Leu Asn Val
1 5 10 15

Ser Met Ala Gly Leu Asn Ser His Pro Ser Ala Val Pro Gln Thr Ser
20 25 30

Met Lys Gln Phe Gln Gly Met Pro Pro Cys Thr Tyr Thr Met Pro Ser
35 40 45

Gln Phe Leu Pro Gln Gln Ala Thr Tyr Phe Pro Pro Ser Pro Pro Ser
50 55 60

Ser Glu Pro Gly Ser Pro Asp Arg Gln Ala Glu Met Leu Gln Asn Leu
65 70 75 80

Thr Pro Pro Pro Ser Tyr Ala Ala Thr Ile Ala Ser Lys Leu Ala Ile
85 90 95

His Asn Pro Asn Leu Pro Ala Thr Leu Pro Val Asn Ser Pro Asn Ile
100 105 110

Gln Pro Val Arg Tyr Asn Arg Arg Ser Asn Pro Asp Leu Glu Lys Arg
115 120 125

```
Arg Ile His Phe Cys Asp Tyr Asp Gly Cys Thr Lys Val Tyr Thr Lys
    130                 135                 140

Ser Ser His Leu Lys Ala His Leu Arg Thr His Thr Gly Glu Lys Pro
145                 150                 155                 160

Tyr Lys Cys Thr Trp Glu Gly Cys Asp Trp Arg Phe Ala Arg Ser Asp
                165                 170                 175

Glu Leu Thr Arg His Tyr Arg Lys His Thr Gly Ala Lys Pro Phe Gln
            180                 185                 190

Cys Val Val Cys Asn Arg Ser Phe Ser Arg Ser Asp His Leu Ala Leu
        195                 200                 205

His Met Lys Arg His Gln Asn
    210                 215
```

<210> 39
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:MAST205b PCR
Forward primer 110F

<400> 39
acagcagtcc tggcactcct t 21

<210> 40
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:MAST205b PCR
Reverse primer 174R

<400> 40
gcggttactt gtccgacaac tc 22

<210> 41
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:MAST205b PCR
Taqman Probe Probe133

<400> 41
tccagccgcc cactgccg 18

<210> 42
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:MAST205 PCR
Forward primer 717F

<400> 42
ttggacagtc tgcaccttct ctta 24

<210> 43
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:MAST205 PCR
Reverse primer 801R

<400> 43
cggttacttg tccgacaaaa gc 22

<210> 44
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:MAST205 PCR
Taqman Probe Probe745

<400> 44
tggcctgaag gacttgagcc ttccagccca ctgccg 36

<210> 45
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hexahistidine
(His) affinity tag

<400> 45
His His His His His His
1 5

<210> 46
<211> 200
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:poly-Gly
flexible linker

<220>
<221> MOD_RES
<222> (6)..(200)
<223> Gly residues from position 6 to 200 may be present
or absent

<400> 46

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Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
  1               5                  10                  15

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
             20                  25                  30

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
         35                  40                  45

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
     50                  55                  60

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 65                  70                  75                  80

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
                 85                  90                  95

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
            100                 105                 110

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
        115                 120                 125

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
    130                 135                 140

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
145                 150                 155                 160

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
                165                 170                 175

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
            180                 185                 190

Gly Gly Gly Gly Gly Gly Gly Gly
        195                 200
```